SEQUENCE LISTING

<110> Bartha, Gabor
      Walker, Michael

<120>
    METHODS FOR ANALYZING GENE EXPRESSION PATTERNS

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<151> 2000-11-01

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Glu Met Phe Arg Thr Cys Gln Phe Cys Pro Gln Phe Arg Glu Ile Ile
    50                  55                  60
His Lys Ala Leu Ile Asp Arg Asn Ile Gln Ala Thr Leu Glu Ser Gln
65                  70                  75                  80
Lys Lys Leu Asn Trp Cys Arg Glu Val Arg Lys Leu Val Ala Leu Lys
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Thr Asn Gly Asp Gly Asn Cys Leu Met His Ala Thr Ser Gln Tyr Met
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Trp Gly Val Gln Asp Thr Asp Leu Val Leu Arg Lys Ala Leu Phe Ser
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Thr Leu Lys Glu Thr Asp Thr Arg Asn Phe Lys Phe Arg Trp Gln Leu
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Glu Ser Leu Lys Ser Gln Glu Phe Val Glu Thr Gly Leu Cys Tyr Asp
145                 150                 155                 160
Thr Arg Asn Trp Asn Asp Glu Trp Asp Asn Leu Ile Lys Met Ala Ser
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Thr Asp Thr Pro Met Ala Arg Ser Gly Leu Gln Tyr Asn Ser Leu Glu
            180                 185                 190
Glu Ile His Ile Phe Val Leu Cys Asn Ile Leu Arg Arg Pro Ile Ile
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Val Ile Ser Asp Lys Met Leu Arg Ser Leu Glu Ser Gly Ser Asn Phe
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Ala Pro Leu Lys Val Gly Gly Ile Tyr Leu Pro Leu His Trp Pro Ala
225                 230                 235                 240
Gln Glu Cys Tyr Arg Tyr Pro Ile Val Leu Gly Tyr Asp Ser His His
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Phe Val Pro Leu Val Thr Leu Lys Asp Ser Gly Pro Glu Ile Arg Ala
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Val Pro Leu Val Asn Arg Asp Arg Gly Arg Phe Glu Asp Leu Lys Val
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His Phe Leu Thr Asp Pro Glu Asn Glu Met Lys Glu Lys Leu Leu Lys
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Glu Tyr Leu Met Val Ile Glu Ile Pro Val Gln Gly Trp Asp His Gly
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Thr Thr His Leu Ile Asn Ala Ala Lys Leu Asp Glu Ala Asn Leu Pro
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Lys Glu Ile Asn Leu Val Asp Asp Tyr Phe Glu Leu Val Gln His Glu
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Tyr Lys Lys Trp Gln Glu Asn Ser Glu Gln Gly Arg Arg Glu Gly His
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385                 390                 395                 400
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Arg Cys His Asn Ala Arg Gln Leu His Ala Ser His Ala Pro Asp His
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Thr Arg His Leu Asp Pro Gly Lys Cys Gln Ala Cys Leu Gln Asp Val
    515                    520                    525
Thr Arg Thr Phe Asn Gly Ile Cys Ser Thr Cys Phe Lys Arg Thr Thr
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Ala Glu Ala Ser Ser Ser Leu Ser Thr Ser Leu Pro Pro Ser Cys His
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Gln Arg Ser Lys Ser Asp Pro Ser Arg Leu Val Arg Ser Pro Ser Pro
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Gln Ala Ala Arg Thr Pro Gly Asp Arg Thr Gly Thr Ser Lys Cys Arg
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Lys Ala Gly Cys Val Tyr Phe Gly Thr Pro Glu Asn Lys Gly Phe Cys
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Ser Gly Lys Val Ser Pro Thr Ala Ser Arg Phe Gln Asn Thr Ile Pro
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Cys Leu Gly Arg Glu Cys Gly Thr Leu Gly Ser Thr Met Phe Glu Gly
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Tyr Cys Gln Lys Cys Phe Ile Glu Ala Gln Asn Gln Arg Phe His Glu
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Ala Lys Arg Thr Glu Glu Gln Leu Arg Ser Ser Gln Arg Arg Asp Val
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Cys Lys Asn Ile Leu Ala Cys Arg Ser Glu Glu Leu Cys Met Glu Cys
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Gln His Pro Asn Gln Arg Met Gly Pro Gly Ala His Arg Gly Glu Pro
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Ala Gly Ala Pro Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
        35   40   45
Leu Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser
    50   55   60
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
65   70   75   80
Gly Gln Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile
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        35                  40                  45
Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
    50                  55                  60
Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro
65                  70                  75                  80
Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala
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        35                  40                  45
Asp Gly Pro Glu Ser Gln Phe Cys Pro Asn Gln Ser Leu Val Ser Leu
    50                  55                  60
Leu Gly Asp Gln Arg Glu Ser Glu Asn Ile Ala Asn Pro Met Gln Thr
65                  70                  75                  80
Ser Ser Ser Val Gln Gln Gln Asn Asp Ala His Leu His Ser Phe Ser
                85                  90                  95
Met Met Pro Ser Ser Ala Cys Glu Ala Met Val Gly His Glu Met Ala
            100                 105                 110
Ser Asp Ser Ser Asn Thr Ser Leu Pro Phe Ser Asn Met Gly Asn Pro
        115                 120                 125
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145                 150                 155                 160
Lys Asp Ala Asp Gly Asp Thr Phe Leu His Ile Ala Val Ala Gln Gly
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Arg Arg Ala Leu Ser Tyr Val Leu Ala Arg Lys Met Asn Ala Leu His
                180                 185                 190
Met Leu Asp Ile Lys Glu His Asn Gly Gln Ser Ala Phe Gln Val Ala
                195                 200                 205
Val Ala Ala Asn Gln His Leu Ile Val Gln Asp Leu Val Asn Ile Gly
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Ala Gln Val Asn Thr Thr Asp Cys Trp Gly Arg Thr Pro Leu His Val
225                 230                 235                 240
Cys Ala Glu Lys Gly His Ser Gln Val Leu Gln Ala Ile Gln Lys Gly
                245                 250                 255
Ala Val Gly Ser Asn Gln Phe Val Asp Leu Glu Ala Thr Asn Tyr Asp
                260                 265                 270
Gly Leu Thr Pro Leu His Cys Ala Val Ile Ala His Asn Ala Val Val
                275                 280                 285
His Glu Leu Gln Arg Asn Gln Gln Pro His Ser Pro Glu Val Gln Glu
    290                 295                 300
Leu Leu Leu Lys Asn Lys Ser Leu Val Asp Thr Ile Lys Cys Leu Ile
305                 310                 315                 320
Gln Met Gly Ala Ala Val Glu Ala Lys Ala Tyr Asn Gly Asn Thr Ala
                325                 330                 335
Leu His Val Ala Ala Ser Leu Gln Tyr Arg Leu Thr Gln Leu Asp Ala
                340                 345                 350
Val Arg Leu Leu Met Arg Lys Gly Ala Asp Pro Ser Thr Arg Asn Leu
                355                 360                 365
Glu Asn Glu Gln Pro Val His Leu Val Pro Asp Gly Pro Val Gly Glu
    370                 375                 380
Gln Ile Arg Arg Ile Leu Lys Gly Lys Ser Ile Gln Gln Arg Ala Pro
385                 390                 395                 400
Pro Tyr
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<210> 9
<211> 1057
<212> DNA
<213> Human

<400> 9
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gcgctgctgc tcctgctcct ggtagccgct ggccggcgcg cagcaggagc gtccgtggcc 180
actgaactgc gctgccagtg cttgcagacc ctgcaggaa ttcaccccaa gaacatccaa 240
agtgtgaacg tgaagtcccc cggaccccac tgcgcccaaa ccgaagtcat agccacactc 300
aagaatgggc ggaaagcttg cctcaatcct gcatccccca tagttaagaa aatcatcgaa 360
aagatgctga acagtgacaa atccaactga ccagaaggga ggaggaagct cactggtggc 420
tgttcctgaa ggaggccctg cccttatagg aacagaagag gaaagagaga cacagctgca 480
gaggccacct ggattgtgcc taatgtgttt gagcatcgct taggagaagt cttctattta 540
tttatttatt cattagtttt gaagattcta tgttaatatt ttaggtgtaa aataattaag 600
ggtatgatta actctacctg cacactgtcc tattatattc attcttttg aaatgtcaac 660
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cccaagttag ttcaatctgg attcatattt aatttgaagg tagaatgttt tcaaatgttc 720
tccagtcatt atgttaatat ttctgaggag cctgcaacat gccagccact gtgatagagg 780
ctggcggatc caagcaaatg gccaatgaga tcattgtgaa ggcaggggaa tgtatgtgca 840
catctgtttt gtaactgttt agatgaatgt cagttgttat ttattgaaat gatttcacag 900
tgtgtggtca acatttctca tgttgaaact ttaagaacta aaatgttcta aatatccctt 960
ggacatttta tgtctttctt gtaaggcata ctgccttgtt taatggtagt tttacagtgt 1020
ttctggctta gaacaaaggg gcttaattat tgatgtt                           1057
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<210> 10
<211> 107
<212> PRT
<213> Human

<400> 10

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Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
1               5                   10                  15
Arg Val Ala Leu Leu Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala
            20                  25                  30
Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
        35                  40                  45
Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
    50                  55                  60
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
65                  70                  75                  80
Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
                85                  90                  95
Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
                100                 105
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<210> 11
<211> 794
<212> DNA
<213> Human

<220>
<221> misc_feature
<222> 7, 14, 22, 35, 37
<223> n = A,T,C or G

<221> misc_feature
<222> 7, 14, 22, 35, 37
<223> n = A,T,C or G

<400> 11
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gatatattta caggctggct caggactatc tgcagtgcgt cctacagata ccacaacctg 180
gatcaggtcc aagcaaaacg tccagagtgc tacaaaatgt tgcgttctca gtccaaaaag 240
aagtggaaaa gaatctgaag tcatgcttgg acaatgttaa tgttgtgtcc gtagacactg 300
ccagaacact attcaaccaa gtgatggaaa aggagtttga agacgacatc attaactggg 360
gaagaattgt aaccatattt gcatttgaag gtattctcat caagaaactt ctacgacagc 420
aaattgcccc ggatgtggat acctataagg agatttcata ttttgttgcg gagttcataa 480
tgaataacac aggagaatgg ataaggcaaa acggaggctg ggaaaatggc tttgtaaaga 540
agtttgaacc taaatctggc tggatgactt ttctagaagt tacaggaaag atctgtgaaa 600
```

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tgctatctct cctgaagcaa tactgttgac cagaaaggac actccatatt gtgaaaccgg 660
cctaattttt ctgactgata tggaaacgat tgccaacaca tacttctact tttaaataaa 720
caactttgat gatgtaactt gaccttccag agttatggaa attttgtccc catgtaatgg 780
                                                                  794
aataaattgt atgt

<210> 12
<211> 175
<212> PRT
<213> Human

<400> 12
Met Thr Asp Cys Glu Phe Gly Tyr Ile Tyr Arg Leu Ala Gln Asp Tyr
1   5   10   15
Leu Gln Cys Val Leu Gln Ile Pro Gln Pro Gly Ser Gly Pro Ser Lys
            20   25   30
Thr Ser Arg Val Leu Gln Asn Val Ala Phe Ser Val Gln Lys Glu Val
        35   40   45
Glu Lys Asn Leu Lys Ser Cys Leu Asp Asn Val Asn Val Val Ser Val
    50   55   60
Asp Thr Ala Arg Thr Leu Phe Asn Gln Val Met Glu Lys Glu Phe Glu
65   70   75   80
Asp Asp Ile Ile Asn Trp Gly Arg Ile Val Thr Ile Phe Ala Phe Glu
                85   90   95
Gly Ile Leu Ile Lys Lys Leu Leu Arg Gln Gln Ile Ala Pro Asp Val
            100   105   110
Asp Thr Tyr Lys Glu Ile Ser Tyr Phe Val Ala Glu Phe Ile Met Asn
        115   120   125
Asn Thr Gly Glu Trp Ile Arg Gln Asn Gly Gly Trp Glu Asn Gly Phe
    130   135   140
Val Lys Lys Phe Glu Pro Lys Ser Gly Trp Met Thr Phe Leu Glu Val
145   150   155   160
Thr Gly Lys Ile Cys Glu Met Leu Ser Leu Leu Lys Gln Tyr Cys
                165   170   175

<210> 13
<211> 800
<212> DNA
<213> Human

<400> 13
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tcaggcagga gaaccaggct ctgctgccac cgagtcccta gccccaactc aacaaacctg 180
aaaggacatc atgtgaggct ctgtaaacca tgcaagcttg agccagagcc cgcctttgg 240
gtggtgcctg gggcactccc acaggtgtag cactcccaaa gcaagactcc agacagcgga 300
gaacctcatg cctggcacct gaggtaccca gcagcctcct gtctcccctt tcagccttca 360
cagcagtgag ctgcaatgtt ggagggcttc atctcgggct gcaaggaccc tgggaaagtt 420
ccagaactcc acgtccttgt ctcaattgtg ccatcaactt tcagagctat catgagccaa 480
cctcacccca cagggcctca gtcgccacca tgtgggcctc tccagtgcaa accaccgagc 540
attccaccat gaccggtcac agctacaaat ccagagacca tcaatcctgc tagagtgcag 600
ggtggcaagc acccaagggt ggctgaccaa gactgcagag tctcctccat cttcaggtcc 660
attcagcctc ctggcattta actaccagca tccagtggtc cccaggaat cccttcctag 720
cctcctgaca tgagtctgct ggaaagagca tccaaacaaa caagtaataa ataaataat 780
                                                                  800
aaactcaaaa aaaaaaaaaa

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<210> 14
<211> 81
<212> PRT
<213> Human

<400> 14
Met Arg Leu Leu Val Leu Ser Ser Leu Leu Cys Ile Leu Leu Leu Cys
1   5   10   15
Phe Ser Ile Phe Ser Thr Glu Gly Lys Arg Arg Pro Ala Lys Ala Trp
            20   25   30
Ser Gly Arg Arg Thr Arg Leu Cys Cys His Arg Val Pro Ser Pro Asn
        35   40   45
Ser Thr Asn Leu Lys Gly His His Val Arg Leu Cys Lys Pro Cys Lys
    50   55   60
Leu Glu Pro Glu Pro Arg Leu Trp Val Val Pro Gly Ala Leu Pro Gln
65   70   75   80
Val

<210> 15
<211> 3169
<212> DNA
<213> Human

<400> 15
gccaggaata actagagagg aacaatgggg ttattcagag gttttgtttt cctcttagtt 60
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gatattgtca ttgttataga tcctagtgtg ccagaagatg aaaaaataat tgaacaaata 180
gaggatatgg tgactacagc ttctacgtac ctgtttgaag ccacagaaaa aagatttttt 240
ttcaaaaatg tatctatatt aattcctgag aattggaagg aaaatcctca gtacaaaagg 300
ccaaaacatg aaaaccataa acatgctgat gttatagttg caccacctac actcccaggt 360
agagatgaac catacaccaa gcagttcaca gaatgtggag agaaaggcga atacattcac 420
ttcacccctg accttctact tggaaaaaaa caaaatgaat atggaccacc aggcaaactg 480
tttgtccatg agtgggctca cctccggtgg ggagtgtttg atgagtacaa tgaagatcag 540
cctttctacc gtgctaagtc aaaaaaaatc gaagcaacaa ggtgttccgc aggtatctct 600
ggtagaaata gagtttataa gtgtcaagga ggcagctgtc ttagtagagc atgcagaatt 660
gattctacaa caaaactgta tggaaaagat tgtcaattct ttcctgataa agtacaaaca 720
gaaaaagcat ccataatgtt tatgcaaagt attgattctg ttgttgaatt ttgtaacgaa 780
aaaacccata atcaagaagc tccaagccta caaaacataa agtgcaattt tagaagtaca 840
tgggaggtga ttagcaattc tgaggatttt aaaaacacca tacccatggt gacaccacct 900
cctccacctg tcttctcatt gctgaagatc agtcaaagaa ttgtgtgctt agttcttgat 960
aagtctggaa gcatgggggg taaggaccgc ctaaatcgaa tgaatcaagc agcaaaacat 1020
ttcctgctgc agactgttga aaatggatcc tgggtgggga tggttcactt tgatagtact 1080
gccactattg taaataagct aatccaaata aaaagcagtg atgaaagaaa cacactcatg 1140
gcaggattac ctacatatcc tctgggagga acttccatct gctctggaat taaatatgca 1200
tttcaggtga ttggagagct acattcccaa ctcgatggat ccgaagtact gctgctgact 1260
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acaggaggaa gtcattttta tgtttcagat gaagctcaga acaatggcct cattgatgct 1440
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aagggattaa cactgaatag taatgcctgg atgaacgaca ctgtcataat tgatagtaca 1560
gtgggaaagg acacgttctt tctcatcaca tggaacagtc tgcctcccag tatttctctc 1620
tgggatccca gtggaacaat aatggaaaat ttcacagtgg atgcaacttc caaaatggcc 1680

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tatctcagta ttccaggaac tgcaaaggtg ggcacttggg catacaatct tcaagccaaa 1740
gcgaacccag aaacattaac tattacagta acttctcgag cagcaaattc ttctgtgcct 1800
ccaatcacag tgaatgctaa aatgaataag gacgtaaaca gtttccccag cccaatgatt 1860
gtttacgcag aaattctaca aggatatgta cctgttcttg gagccaatgt gactgctttc 1920
attgaatcac agaatggaca tacagaagtt ttggaacttt tggataatgg tgcaggcgct 1980
gattctttca agaatgatgg agtctactcc aggtatttta cagcatatac agaaaatggc 2040
agatatagct taaaagttcg ggctcatgga ggagcaaaca ctgccaggct aaaattacgg 2100
cctccactga atagagccgc gtacatacca ggctgggtag tgaacgggga aattgaagca 2160
aacccgccaa gacctgaaat tgatgaggat actcagacca ccttggagga tttcagccga 2220
acagcatccg gaggtgcatt tgtggtatca caagtcccaa gccttccctt gcctgaccaa 2280
tacccaccaa gtcaaatcac agaccttgat gccacagttc atgaggataa gattattctt 2340
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ataagtgcaa gtattcttga tctaagagac agttttgatg atgctcttca agtaaatact 2460
actgatctgt caccaaagga ggccaactcc aaggaaagct ttgcatttaa accagaaaat 2520
atctcagaag aaaatgcaac ccacatattt attgccatta aagtataga taaaagcaat 2580
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gatgacattg atcctactcc tactcctact cctactcctg ataaaagtca taattctgga 2700
gttaatattt ctacgctggt attgtctgtg attgggtctg ttgtaattgt aacttttatt 2760
ttaagtacca ccatttgaac cttaacgaag aaaaaaatct tcaagtagac ctagaagaga 2820
gttttaaaaa acaaaacaat gtaagtaaag gatatttctg aatcttaaaa ttcatcccat 2880
gtgtgatcat aaactcataa aaataatttt aagatgtcgg aaaaggatac tttgattaaa 2940
taaaaacact catggatatg taaaaactgt caagattaaa atttaatagt ttcatttatt 3000
tgttatttta tttgtaagaa atagtgatga acaaagatcc tttttcatac tgatacctgg 3060
ttgtatatta tttgatgcaa cagttttctg aaatgatatt tcaaattgca tcaagaaatt 3120
aaaatcatct atctgagtag tcaaaataca agtaaaggag agcaaataa            3169


<210> 16
<211> 917
<212> PRT
<213> Human

<400> 16
Met Gly Leu Phe Arg Gly Phe Val Phe Leu Leu Val Leu Cys Leu Leu
1               5                   10                  15
His Gln Ser Asn Thr Ser Phe Ile Lys Leu Asn Asn Asn Gly Phe Glu
            20                  25                  30
Asp Ile Val Ile Val Ile Asp Pro Ser Val Pro Glu Asp Glu Lys Ile
        35                  40                  45
Ile Glu Gln Ile Glu Asp Met Val Thr Thr Ala Ser Thr Tyr Leu Phe
    50                  55                  60
Glu Ala Thr Glu Lys Arg Phe Phe Phe Lys Asn Val Ser Ile Leu Ile
65                  70                  75                  80
Pro Glu Asn Trp Lys Glu Asn Pro Gln Tyr Lys Arg Pro Lys His Glu
                85                  90                  95
Asn His Lys His Ala Asp Val Ile Val Ala Pro Pro Thr Leu Pro Gly
            100                 105                 110
Arg Asp Glu Pro Tyr Thr Lys Gln Phe Thr Glu Cys Gly Glu Lys Gly
        115                 120                 125
Glu Tyr Ile His Phe Thr Pro Asp Leu Leu Leu Gly Lys Lys Gln Asn
    130                 135                 140
Glu Tyr Gly Pro Pro Gly Lys Leu Phe Val His Glu Trp Ala His Leu
145                 150                 155                 160
Arg Trp Gly Val Phe Asp Glu Tyr Asn Glu Asp Gln Pro Phe Tyr Arg
                165                 170                 175
Ala Lys Ser Lys Lys Ile Glu Ala Thr Arg Cys Ser Ala Gly Ile Ser
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                    180                      185                      190
Gly Arg Asn Arg Val Tyr Lys Cys Gln Gly Gly Ser Cys Leu Ser Arg
          195                      200                      205
Ala Cys Arg Ile Asp Ser Thr Thr Lys Leu Tyr Gly Lys Asp Cys Gln
          210                      215                      220
Phe Phe Pro Asp Lys Val Gln Thr Glu Lys Ala Ser Ile Met Phe Met
225                      230                      235                      240
Gln Ser Ile Asp Ser Val Val Glu Phe Cys Asn Glu Lys Thr His Asn
                    245                      250                      255
Gln Glu Ala Pro Ser Leu Gln Asn Ile Lys Cys Asn Phe Arg Ser Thr
          260                      265                      270
Trp Glu Val Ile Ser Asn Ser Glu Asp Phe Lys Asn Thr Ile Pro Met
          275                      280                      285
Val Thr Pro Pro Pro Pro Pro Val Phe Ser Leu Leu Lys Ile Ser Gln
          290                      295                      300
Arg Ile Val Cys Leu Val Leu Asp Lys Ser Gly Ser Met Gly Gly Lys
305                      310                      315                      320
Asp Arg Leu Asn Arg Met Asn Gln Ala Ala Lys His Phe Leu Leu Gln
                    325                      330                      335
Thr Val Glu Asn Gly Ser Trp Val Gly Met Val His Phe Asp Ser Thr
          340                      345                      350
Ala Thr Ile Val Asn Lys Leu Ile Gln Ile Lys Ser Ser Asp Glu Arg
          355                      360                      365
Asn Thr Leu Met Ala Gly Leu Pro Thr Tyr Pro Leu Gly Gly Thr Ser
          370                      375                      380
Ile Cys Ser Gly Ile Lys Tyr Ala Phe Gln Val Ile Gly Glu Leu His
385                      390                      395                      400
Ser Gln Leu Asp Gly Ser Glu Val Leu Leu Leu Thr Asp Gly Glu Asp
                    405                      410                      415
Asn Thr Ala Ser Ser Cys Ile Asp Glu Val Lys Gln Ser Gly Ala Ile
          420                      425                      430
Val His Phe Ile Ala Leu Gly Arg Ala Ala Asp Glu Ala Val Ile Glu
          435                      440                      445
Met Ser Lys Ile Thr Gly Gly Ser His Phe Tyr Val Ser Asp Glu Ala
450                      455                      460
Gln Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala Leu Thr Ser Gly Asn
465                      470                      475                      480
Thr Asp Leu Ser Gln Lys Ser Leu Gln Leu Glu Ser Lys Gly Leu Thr
                    485                      490                      495
Leu Asn Ser Asn Ala Trp Met Asn Asp Thr Val Ile Ile Asp Ser Thr
          500                      505                      510
Val Gly Lys Asp Thr Phe Phe Leu Ile Thr Trp Asn Ser Leu Pro Pro
          515                      520                      525
Ser Ile Ser Leu Trp Asp Pro Ser Gly Thr Ile Met Glu Asn Phe Thr
          530                      535                      540
Val Asp Ala Thr Ser Lys Met Ala Tyr Leu Ser Ile Pro Gly Thr Ala
545                      550                      555                      560
Lys Val Gly Thr Trp Ala Tyr Asn Leu Gln Ala Lys Ala Asn Pro Glu
                    565                      570                      575
Thr Leu Thr Ile Thr Val Thr Ser Arg Ala Ala Asn Ser Ser Val Pro
          580                      585                      590
Pro Ile Thr Val Asn Ala Lys Met Asn Lys Asp Val Asn Ser Phe Pro
          595                      600                      605
Ser Pro Met Ile Val Tyr Ala Glu Ile Leu Gln Gly Tyr Val Pro Val
          610                      615                      620
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Leu Gly Ala Asn Val Thr Ala Phe Ile Glu Ser Gln Asn Gly His Thr
625   630   635   640
Glu Val Leu Glu Leu Leu Asp Asn Gly Ala Gly Ala Asp Ser Phe Lys
                645   650   655
Asn Asp Gly Val Tyr Ser Arg Tyr Phe Thr Ala Tyr Thr Glu Asn Gly
                660   665   670
Arg Tyr Ser Leu Lys Val Arg Ala His Gly Gly Ala Asn Thr Ala Arg
            675   680   685
Leu Lys Leu Arg Pro Pro Leu Asn Arg Ala Ala Tyr Ile Pro Gly Trp
        690   695   700
Val Val Asn Gly Glu Ile Glu Ala Asn Pro Pro Arg Pro Glu Ile Asp
705   710   715   720
Glu Asp Thr Gln Thr Thr Leu Glu Asp Phe Ser Arg Thr Ala Ser Gly
                725   730   735
Gly Ala Phe Val Val Ser Gln Val Pro Ser Leu Pro Leu Pro Asp Gln
                740   745   750
Tyr Pro Pro Ser Gln Ile Thr Asp Leu Asp Ala Thr Val His Glu Asp
            755   760   765
Lys Ile Ile Leu Thr Trp Thr Ala Pro Gly Asp Asn Phe Asp Val Gly
    770   775   780
Lys Val Gln Arg Tyr Ile Ile Arg Ile Ser Ala Ser Ile Leu Asp Leu
785   790   795   800
Arg Asp Ser Phe Asp Asp Ala Leu Gln Val Asn Thr Thr Asp Leu Ser
                805   810   815
Pro Lys Glu Ala Asn Ser Lys Glu Ser Phe Ala Phe Lys Pro Glu Asn
            820   825   830
Ile Ser Glu Glu Asn Ala Thr His Ile Phe Ile Ala Ile Lys Ser Ile
            835   840   845
Asp Lys Ser Asn Leu Thr Ser Lys Val Ser Asn Ile Ala Gln Val Thr
            850   855   860
Leu Phe Ile Pro Gln Ala Asn Pro Asp Asp Ile Asp Pro Thr Pro Thr
865   870   875   880
Pro Thr Pro Thr Pro Asp Lys Ser His Asn Ser Gly Val Asn Ile Ser
                885   890   895
Thr Leu Val Leu Ser Val Ile Gly Ser Val Val Ile Val Asn Phe Ile
            900   905   910
Leu Ser Thr Thr Ile
        915

<210> 17
<211> 737
<212> DNA
<213> Human

<400> 17
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actgtcagcc ccagaatgtt gacagtcgct ctcctagccc ttctctgtgc ctcagcctct 180
ggcaatgcca ttcaggccag gtcttcctcc tatagtggag agtatggaag tggtggtgga 240
aagcgattct ctcattctgg caaccagttg gacggcccca tcaccgccct ccgggtccga 300
gtcaacacat actacatcgt aggtcttcag gtgcgctatg caaggtgtg gagcgactat 360
gtgggtggtc gcaacggaga cctggaggag atctttctgc accctgggga atcagtgatc 420
caggtttctg ggaagtacaa gtggtacctg aagaagctgg tatttgtgac agacaagggc 480
cgctatctgt cttttgggaa agacagtggc acaagtttca atgccgtccc cttgcacccc 540

aacaccgtgc tccgcttcat cagtggccgg tctggttctc tcatcgatgc cattggcctg 600
cactgggatg tttaccccac tagctgcagc agatgctgag cctcctctcc ttggcagggg 660
cactgtgatg aggagtaaga actcccttat cactaacccc catccaaatg gctcaataaa 720
aaaatatggt taaggct 737

<210> 18
<211> 198
<212> PRT
<213> Human

<400> 18
Met Ser Cys Pro His Arg Asp Leu Pro Ser Ala His Cys Glu Asn Trp
1   5   10   15
Lys Phe Pro Gly Gly Cys Phe Ala Ser Glu Thr Val Ser Pro Arg Met
            20   25   30
Leu Thr Val Ala Leu Leu Ala Leu Leu Cys Ala Ser Ala Ser Gly Asn
        35   40   45
Ala Ile Gln Ala Arg Ser Ser Ser Tyr Ser Gly Glu Tyr Gly Ser Gly
    50   55   60
Gly Gly Lys Arg Phe Ser His Ser Gly Asn Gln Leu Asp Gly Pro Ile
65   70   75   80
Thr Ala Leu Arg Val Arg Val Asn Thr Tyr Tyr Ile Val Gly Leu Gln
                85   90   95
Val Arg Tyr Gly Lys Val Trp Ser Asp Tyr Val Gly Gly Arg Asn Gly
            100   105   110
Asp Leu Glu Glu Ile Phe Leu His Pro Gly Glu Ser Val Ile Gln Val
        115   120   125
Ser Gly Lys Tyr Lys Trp Tyr Leu Lys Lys Leu Val Phe Val Thr Asp
    130   135   140
Lys Gly Arg Tyr Leu Ser Phe Gly Lys Asp Ser Gly Thr Ser Phe Asn
145   150   155   160
Ala Val Pro Leu His Pro Asn Thr Val Leu Arg Phe Ile Ser Gly Arg
                165   170   175
Ser Gly Ser Leu Ile Asp Ala Ile Gly Leu His Trp Asp Val Tyr Pro
            180   185   190
Thr Ser Cys Ser Arg Cys
            195

<210> 19
<211> 2879
<212> DNA
<213> Human

<400> 19
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aagaagtgtt caccacatag ttgcaaaggt cttcaacttg ccacagccaa cagaaaaatc 180
aaaatgattg aaccctttgg gaatcagtat attgtggcca ggccagtgta ttctacaaat 240
gcttttgagg aaaatcataa aaagacagga agacatcata agacatttct ggatcatctc 300
aaagtgtgtt gtagctgttc cccacaaaag gccaagagaa ttgtcctctc tttgttcccc 360
atagcatctt ggttgccagc ataccggctt aaagaatggt tgctcagtga tattgtttct 420
ggtatcagca cagggattgt ggccgtacta caaggtttag catttgctct gctggtcgac 480
attcccccag tctatgggtt gtatgcatcc tttttcccag ccataatcta ccttttcttc 540
ggcacttcca gacacatatc cgtgggtccg tttccgattc tgagtatgat ggtgggacta 600

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gcagtttcag gagcagtttc aaaagcagtc ccagatcgca atgcaactac tttgggattg 660
cctaacaact cgaataattc ttcactactg gatgacgaga gggtgagggt ggcggcggcg 720
gcatcagtca cagtgctttc tggaatcatc cagttggctt ttgggattct cgcggattgga 780
tttgtagtga tatacctgtc tgagtccctc atcagtggct tcactactgc tgctgctgtt 840
catgtttttgg tttcccaact caaattcatt tttcagttga cagtcccgtc acacactgat 900
ccagtttcaa tttttcaaagt actatactct gtattctcac aaatagagaa gactaatatt 960
gcagacctgg tgacagctct gattgtcctt ttggttgtat ccattgttaa agaaataaat 1020
cagcgcttca aagacaaact tccagtgccc attccaatcg aattcattat gaccgtgatt 1080
gcagcaggtg tatcctacgg ctgtgacttt aaaaacaggt ttaaagtggc tgtggttggg 1140
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<210> 20
<211> 764
<212> PRT
<213> Human

<400> 20
Met Ile Glu Pro Phe Gly Asn Gln Tyr Ile Val Ala Arg Pro Val Tyr
1               5                   10                  15
Ser Thr Asn Ala Phe Glu Glu Asn His Lys Lys Thr Gly Arg His His
            20                  25                  30
Lys Thr Phe Leu Asp His Leu Lys Val Cys Cys Ser Cys Ser Pro Gln
        35                  40                  45
Lys Ala Lys Arg Ile Val Leu Ser Leu Phe Pro Ile Ala Ser Trp Leu
    50                  55                  60
Pro Ala Tyr Arg Leu Lys Glu Trp Leu Leu Ser Asp Ile Val Ser Gly
65                  70                  75                  80
```

```
Ile Ser Thr Gly Ile Val Ala Val Leu Gln Gly Leu Ala Phe Ala Leu
                 85                    90                    95
Leu Val Asp Ile Pro Pro Val Tyr Gly Leu Tyr Ala Ser Phe Phe Pro
               100                  105                  110
Ala Ile Ile Tyr Leu Phe Phe Gly Thr Ser Arg His Ile Ser Val Gly
           115                  120                  125
Pro Phe Pro Ile Leu Ser Met Met Val Gly Leu Ala Val Ser Gly Ala
       130                  135                  140
Val Ser Lys Ala Val Pro Asp Arg Asn Ala Thr Thr Leu Gly Leu Pro
145                  150                  155                  160
Asn Asn Ser Asn Asn Ser Ser Leu Leu Asp Asp Glu Arg Val Arg Val
               165                  170                  175
Ala Ala Ala Ala Ser Val Thr Val Leu Ser Gly Ile Ile Gln Leu Ala
           180                  185                  190
Phe Gly Ile Leu Arg Ile Gly Phe Val Val Ile Tyr Leu Ser Glu Ser
       195                  200                  205
Leu Ile Ser Gly Phe Thr Thr Ala Ala Ala Val His Val Leu Val Ser
   210                  215                  220
Gln Leu Lys Phe Ile Phe Gln Leu Thr Val Pro Ser His Thr Asp Pro
225                  230                  235                  240
Val Ser Ile Phe Lys Val Leu Tyr Ser Val Phe Ser Gln Ile Glu Lys
               245                  250                  255
Thr Asn Ile Ala Asp Leu Val Thr Ala Leu Ile Val Leu Leu Val Val
           260                  265                  270
Ser Ile Val Lys Glu Ile Asn Gln Arg Phe Lys Asp Lys Leu Pro Val
       275                  280                  285
Pro Ile Pro Ile Glu Phe Ile Met Thr Val Ile Ala Ala Gly Val Ser
   290                  295                  300
Tyr Gly Cys Asp Phe Lys Asn Arg Phe Lys Val Ala Val Val Gly Asp
305                  310                  315                  320
Met Asn Pro Gly Phe Gln Pro Pro Ile Thr Pro Asp Val Glu Thr Phe
               325                  330                  335
Gln Asn Thr Val Gly Asp Cys Phe Gly Ile Ala Met Val Ala Phe Ala
           340                  345                  350
Val Ala Phe Ser Val Ala Ser Val Tyr Ser Leu Lys Tyr Asp Tyr Pro
       355                  360                  365
Leu Asp Gly Asn Gln Glu Leu Ile Ala Leu Gly Leu Gly Asn Ile Val
   370                  375                  380
Cys Gly Val Phe Arg Gly Phe Ala Gly Ser Thr Ala Leu Ser Arg Ser
385                  390                  395                  400
Ala Val Gln Glu Ser Thr Gly Gly Lys Thr Gln Ile Ala Gly Leu Ile
               405                  410                  415
Gly Ala Ile Ile Val Leu Ile Val Val Leu Ala Ile Gly Phe Leu Leu
           420                  425                  430
Ala Pro Leu Gln Lys Ser Val Leu Ala Ala Leu Ala Leu Gly Asn Leu
       435                  440                  445
Lys Gly Met Leu Met Gln Phe Ala Glu Ile Gly Arg Leu Trp Arg Lys
   450                  455                  460
Asp Lys Tyr Asp Cys Leu Ile Trp Ile Met Thr Phe Ile Phe Thr Ile
465                  470                  475                  480
Val Leu Gly Leu Gly Leu Gly Leu Ala Ala Ser Val Ala Phe Gln Leu
               485                  490                  495
Leu Thr Ile Val Phe Arg Thr Gln Phe Pro Lys Cys Ser Thr Leu Ala
               500                  505                  510
Asn Ile Gly Arg Thr Asn Ile Tyr Lys Asn Lys Lys Asp Tyr Tyr Asp
```

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        515                    520                      525
Met Tyr Glu Pro Glu Gly Val Lys Ile Phe Arg Cys Pro Ser Pro Ile
        530                    535                      540
Tyr Phe Ala Asn Ile Gly Phe Phe Arg Arg Lys Leu Ile Asp Ala Val
545                      550                      555             560
Gly Phe Ser Pro Leu Arg Ile Leu Arg Lys Arg Asn Lys Ala Leu Arg
                    565                      570                  575
Lys Ile Arg Lys Leu Gln Lys Gln Gly Leu Leu Gln Val Thr Pro Lys
                580                      585                  590
Gly Phe Ile Cys Thr Val Asp Thr Ile Lys Asp Ser Asp Glu Glu Leu
                595                      600                  605
Asp Asn Asn Gln Ile Glu Val Leu Asp Gln Pro Ile Asn Thr Thr Asp
        610                      615                      620
Leu Pro Phe His Ile Asp Trp Asn Asp Asp Leu Pro Leu Asn Ile Glu
625                      630                      635             640
Val Pro Lys Ile Ser Leu His Ser Leu Ile Leu Asp Phe Ser Ala Val
                    645                      650                  655
Ser Phe Leu Asp Val Ser Ser Val Arg Gly Leu Lys Ser Ile Leu Gln
                660                      665                  670
Glu Phe Ile Arg Ile Lys Val Asp Val Tyr Ile Val Gly Thr Asp Asp
            675                      680                  685
Asp Phe Ile Glu Lys Leu Asn Arg Tyr Glu Phe Phe Asp Gly Glu Val
        690                      695                      700
Lys Ser Ser Ile Phe Phe Leu Thr Ile His Asp Ala Val Leu His Ile
705                      710                      715             720
Leu Met Lys Lys Asp Tyr Ser Thr Ser Lys Phe Asn Pro Ser Gln Glu
                    725                      730                  735
Lys Asp Gly Lys Ile Asp Phe Thr Ile Asn Thr Asn Gly Gly Leu Arg
                740                      745                  750
Asn Arg Val Tyr Glu Val Pro Val Glu Thr Lys Phe
        755                      760
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<210> 21
<211> 655
<212> DNA
<213> Human

<400> 21
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ctctctcggg cactgctgcc atgaatgcct tcctgctctt cgcactgtgc ctccttgggg  120
cctgggccgc cttggcagga ggggtcaccg tgcaggatgg aaatttctcc ttttctctgg  180
agtcagtgaa gaagctcaaa gacctccagg agccccagga gcccagggtt gggaaactca  240
ggaactttgc acccatccct ggtgaacctg tggttcccat cctctgtagc aacccgaact  300
ttccagaaga actcaagcct ctctgcaagg agcccaatgc caggagata cttcagaggc  360
tggaggaaat cgctgaggac ccgggcacat gtgaaatctg tgcctacgct gcctgtaccg  420
gatgctaggg gggcttgccc actgcctgcc tcccctccgc agcagggaag ctcttttctc  480
ctgcagaaag ggccacccat gatactccac tcccagcagc tcaacctacc ctggtccagt  540
cgggaggagc agcccgggga ggaactgggt gactggaggc ctcgccccaa cactgtcctt  600
ccctgccact tcaaccccca gctaataaac cagattccag agtaaaaaaa aaaaa       655
```

<210> 22
<211> 115
<212> PRT
<213> Human

<400> 22
Met Asn Ala Phe Leu Leu Phe Ala Leu Cys Leu Leu Gly Ala Trp Ala
1   5   10   15
Ala Leu Ala Gly Gly Val Thr Val Gln Asp Gly Asn Phe Ser Phe Ser
            20   25   30
Leu Glu Ser Val Lys Lys Leu Lys Asp Leu Gln Glu Pro Gln Glu Pro
        35   40   45
Arg Val Gly Lys Leu Arg Asn Phe Ala Pro Ile Pro Gly Glu Pro Val
    50   55   60
Val Pro Ile Leu Cys Ser Asn Pro Asn Phe Pro Glu Glu Leu Lys Pro
65   70   75   80
Leu Cys Lys Glu Pro Asn Ala Gln Glu Ile Leu Gln Arg Leu Glu Glu
                85   90   95
Ile Ala Glu Asp Pro Gly Thr Cys Glu Ile Cys Ala Tyr Ala Ala Cys
            100   105   110
Thr Gly Cys
        115

<210> 23
<211> 1244
<212> DNA
<213> Human

<400> 23
cagtcctcag gtgcaacccc tgcgtggtct ctgtggcagc cttctctcat tcagagcttg 60
cacagttgca gttagttatt ccaggtatta tttttgtttt cagaaaaaga aaactcagta 120
gaagataatg gcaagtccag actggggata tgatgacaaa aatggtcctg aacaatggag 180
caagctgtat cccattgcca atggaaataa ccagtcccct gttgatatta aaaccagtga 240
aaccaaacat gacacctctc tgaaacctat tagtgtctcc tacaacccag ccacagccaa 300
agaaattatc aatgtggggc attccttcca tgtaaatttt gaggacaacg ataaccgatc 360
agtgctgaaa ggtggtcctt tctctgacag ctacaggctc tttcagttcc attttcactg 420
gggcagtaca aatgagcatg gttcagaaca tacagtggat ggagtcaaat attctgccga 480
gcttcacgta gctcactgga attctgcaaa gtactccagc cttgctgaag ctgcctcaaa 540
ggctgatggt ttggcagtta ttggtgtttt gatgaaggtt ggtgaggcca acccaaagct 600
gcagaaagta cttgatgccc tccaagcaat taaaaccaag ggcaaacgag ccccattcac 660
aaattttgac ccctctactc tccttccttc atccctggat ttctggacct accctggctc 720
tctgactcat cctcctcttt atgagagtgt aacttggatc atctgtaagg agagcatcag 780
tgtcagctca gagcagctgg cacaattccg cagccttcta tcaaatgttg aaggtgataa 840
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agcttcattt tgatgattct gagaagaaac ttgtccttcc tcaagaacac agccctgctt 960
ctgacataat ccagtaaaat aataattttt aagaaataaa tttatttcaa tattagcaag 1020
acagcatgcc ttcaaatcaa tctgtaaaac taagaaactt aaattttagt cttactgct 1080
taattcaaat aataattagt aagctagcaa atagtaatct gtaagcataa gcttatgctt 1140
aaattcaagt ttagtttgag gaattcttta aaattacaac taagtgattt gtatgtctat 1200
tttttttcagt ttatttgaac caataaaata atttttatctc tttc 1244

<210> 24
<211> 261
<212> PRT
<213> Human

<400> 24
Met Ala Ser Pro Asp Trp Gly Tyr Asp Asp Lys Asn Gly Pro Glu Gln

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          1                    5                    10                   15
      Trp Ser Lys Leu Tyr Pro Ile Ala Asn Gly Asn Asn Gln Ser Pro Val
                     20                   25                   30
      Asp Ile Lys Thr Ser Glu Thr Lys His Asp Thr Ser Leu Lys Pro Ile
                35                   40                   45
      Ser Val Ser Tyr Asn Pro Ala Thr Ala Lys Glu Ile Ile Asn Val Gly
           50                   55                   60
      His Ser Phe His Val Asn Phe Glu Asp Asn Asp Asn Arg Ser Val Leu
      65                   70                   75                   80
      Lys Gly Gly Pro Phe Ser Asp Ser Tyr Arg Leu Phe Gln Phe His Phe
                          85                   90                   95
      His Trp Gly Ser Thr Asn Glu His Gly Ser Glu His Thr Val Asp Gly
                     100                  105                  110
      Val Lys Tyr Ser Ala Glu Leu His Val Ala His Trp Asn Ser Ala Lys
                115                  120                  125
      Tyr Ser Ser Leu Ala Glu Ala Ala Ser Lys Ala Asp Gly Leu Ala Val
                130                  135                  140
      Ile Gly Val Leu Met Lys Val Gly Glu Ala Asn Pro Lys Leu Gln Lys
      145                  150                  155                  160
      Val Leu Asp Ala Leu Gln Ala Ile Lys Thr Lys Gly Lys Arg Ala Pro
                     165                  170                  175
      Phe Thr Asn Phe Asp Pro Ser Thr Leu Leu Pro Ser Ser Leu Asp Phe
                     180                  185                  190
      Trp Thr Tyr Pro Gly Ser Leu Thr His Pro Pro Leu Tyr Glu Ser Val
                195                  200                  205
      Thr Trp Ile Ile Cys Lys Glu Ser Ile Ser Val Ser Ser Glu Gln Leu
      210                  215                  220
      Ala Gln Phe Arg Ser Leu Leu Ser Asn Val Glu Gly Asp Asn Ala Val
      225                  230                  235                  240
      Pro Met Gln His Asn Asn Arg Pro Thr Gln Pro Leu Lys Gly Arg Thr
                     245                  250                  255
      Val Arg Ala Ser Phe
                     260
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```
<210> 25
<211> 3111
<212> DNA
<213> Human

<400> 25
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atcttgattc ttcaccttct agaaggggcc ctgagtaatt cactcattca gctgaacaac 120
aatggctatg aaggcattgt cgttgcaatc gaccccaatg tgccagaaga tgaaacactc 180
attcaacaaa taaaggacat ggtgacccag gcatctctgt atctgtttga agctacagga 240
aagcgatttt atttcaaaaa tgttgccatt ttgattcctg aaacatggaa gacaaaggct 300
gactatgtga gaccaaaact tgagacctac aaaaatgctg atgttctggt tgctgagtct 360
actcctccag gtaatgatga accctacact gagcagatgg gcaactgtgg agagaagggt 420
gaaaggatcc acctcactcc tgatttcatt gcaggaaaaa agttagctga atatggacca 480
caaggtaggg catttgtcca tgagtgggct catctacgat ggggagtatt tgacgagtac 540
aataatgatg agaaattcta cttatccaat ggaagaatac aagcagtaag atgttcagca 600
ggtattactg gtacaaatgt agtaaagaag tgtcagggag cagctgtta caccaaaaga 660
tgcacattca ataaagtaac aggactctat gaaaaaggat gtgagtttgt tctccaatcc 720
cgccagacgg agaaggcttc tataatgttt gcacaacatg ttgattctat agttgaattc 780
tgtacagaac aaaaccacaa caaagaagct ccaaacaagc aaaatcaaaa atgcaatctc 840
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cgaagcacat gggaagtgat ccgtgattct gaggacttta agaaaccac tcctatgaca  900
acacagccac caaatcccac cttctcattg ctgcagattg acaaagaat tgtgtgttta  960
gtccttgaca aatctggaag catggcgact ggtaaccgcc tcaatcgact gaatcaagca 1020
ggccagcttt tcctgctgca gacagttgag ctgggtcct gggttgggat ggtgacattt 1080
gacagtgctg cccatgtaca aagtgaactc atacagataa acagtggcag tgacagggac 1140
acactcgcca aaagattacc tgcagcagct tcaggaggga cgtccatctg cagcgggctt 1200
cgatcggcat ttactgtgat taggaagaaa tatccaactg atggatctga aattgtgctg 1260
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gccatcatcc acacagtcgc tttggggccc tctgcagctc aagaactaga ggagctgtcc 1380
aaaatgacag gaggtttaca gacatatgct tcagatcaag ttcagaacaa tggcctcatt 1440
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aacagcacca ttcctggcat tcacatttta aaaattatgt ggaagtggat aggagaactg 2760
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taaaaactat ccattcaaac ccaaaaattt aataatcatt gagtctttta ttaatgaatt 3060
tgaatactag aaagaaacag ggcttgcatc aataaatgga agtatgagtg t           3111
```

<210> 26
<211> 914
<212> PRT
<213> Human

<400> 26

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Met Gly Pro Phe Lys Ser Ser Val Phe Ile Leu Ile Leu His Leu Leu
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Glu Gly Ala Leu Ser Asn Ser Leu Ile Gln Leu Asn Asn Asn Gly Tyr
            20                  25                  30
Glu Gly Ile Val Val Ala Ile Asp Pro Asn Val Pro Glu Asp Glu Thr
        35                  40                  45
Leu Ile Gln Gln Ile Lys Asp Met Val Thr Gln Ala Ser Leu Tyr Leu
    50                  55                  60
Phe Glu Ala Thr Gly Lys Arg Phe Tyr Phe Lys Asn Val Ala Ile Leu
65                  70                  75                  80
```

Ile Pro Glu Thr Trp Lys Thr Lys Ala Asp Tyr Val Arg Pro Lys Leu
                85   90   95

Glu Thr Tyr Lys Asn Ala Asp Val Leu Val Ala Glu Ser Thr Pro Pro
            100   105   110

Gly Asn Asp Glu Pro Tyr Thr Glu Gln Met Gly Asn Cys Gly Glu Lys
            115   120   125

Gly Glu Arg Ile His Leu Thr Pro Asp Phe Ile Ala Gly Lys Lys Leu
  . 130   135   140

Ala Glu Tyr Gly Pro Gln Gly Arg Ala Phe Val His Glu Trp Ala His
145   150   155   160

Leu Arg Trp Gly Val Phe Asp Glu Tyr Asn Asn Asp Glu Lys Phe Tyr
                165   170   175

Leu Ser Asn Gly Arg Ile Gln Ala Val Arg Cys Ser Ala Gly Ile Thr
                180   185   190

Gly Thr Asn Val Val Lys Lys Cys Gln Gly Gly Ser Cys Tyr Thr Lys
                195   200   205

Arg Cys Thr Phe Asn Lys Val Thr Gly Leu Tyr Glu Lys Gly Cys Glu
            210   215   220

Phe Val Leu Gln Ser Arg Gln Thr Glu Lys Ala Ser Ile Met Phe Ala
225   230   235   240

Gln His Val Asp Ser Ile Val Glu Phe Cys Thr Glu Gln Asn His Asn
                245   250   255

Lys Glu Ala Pro Asn Lys Gln Asn Gln Lys Cys Asn Leu Arg Ser Thr
            260   265   270

Trp Glu Val Ile Arg Asp Ser Glu Asp Phe Lys Lys Thr Thr Pro Met
            275   280   285

Thr Thr Gln Pro Pro Asn Pro Thr Phe Ser Leu Leu Gln Ile Gly Gln
    290   295   300

Arg Ile Val Cys Leu Val Leu Asp Lys Ser Gly Ser Met Ala Thr Gly
305   310   315   320

Asn Arg Leu Asn Arg Leu Asn Gln Ala Gly Gln Leu Phe Leu Leu Gln
                325   330   335

Thr Val Glu Leu Gly Ser Trp Val Gly Met Val Thr Phe Asp Ser Ala
            340   345   350

Ala His Val Gln Ser Glu Leu Ile Gln Ile Asn Ser Gly Ser Asp Arg
            355   360   365

Asp Thr Leu Ala Lys Arg Leu Pro Ala Ala Ala Ser Gly Gly Thr Ser
    370   375   380

Ile Cys Ser Gly Leu Arg Ser Ala Phe Thr Val Ile Arg Lys Lys Tyr
385   390   395   400

Pro Thr Asp Gly Ser Glu Ile Val Leu Leu Thr Asp Gly Glu Asp Asn
                405   410   415

Thr Ile Ser Gly Cys Phe Asn Glu Val Lys Gln Ser Gly Ala Ile Ile
            420   425   430

His Thr Val Ala Leu Gly Pro Ser Ala Ala Gln Glu Leu Glu Glu Leu
            435   440   445

Ser Lys Met Thr Gly Gly Leu Gln Thr Tyr Ala Ser Asp Gln Val Gln
    450   455   460

Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala Leu Ser Ser Gly Asn Gly
465   470   475   480

Ala Val Ser Gln Arg Ser Ile Gln Leu Glu Ser Lys Gly Leu Thr Leu
                485   490   495

Gln Asn Ser Gln Trp Met Asn Gly Thr Val Ile Val Asp Ser Thr Val
                500   505   510

Gly Lys Asp Thr Leu Phe Leu Ile Thr Trp Thr Thr Gln Pro Pro Gln

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                515                    520                      525
Ile Leu Leu Trp Asp Pro Ser Gly Gln Lys Gln Gly Gly Phe Val Val
        530                        535                      540
Asp Lys Asn Thr Lys Met Ala Tyr Leu Gln Ile Pro Gly Ile Ala Lys
545                        550                      555              560
Val Gly Thr Trp Lys Tyr Ser Leu Gln Ala Ser Ser Gln Thr Leu Thr
                    565                      570                  575
Leu Thr Val Thr Ser Arg Ala Ser Asn Ala Thr Leu Pro Pro Ile Thr
                580                      585                  590
Val Thr Ser Lys Thr Asn Lys Asp Thr Ser Lys Phe Pro Ser Pro Leu
            595                      600                  605
Val Val Tyr Ala Asn Ile Arg Gln Gly Ala Ser Pro Ile Leu Arg Ala
        610                      615                  620
Ser Val Thr Ala Leu Ile Glu Ser Val Asn Gly Lys Thr Val Thr Leu
625                      630                      635              640
Glu Leu Leu Asp Asn Gly Ala Gly Ala Asp Ala Thr Lys Asp Asp Gly
                    645                      650                  655
Val Tyr Ser Arg Tyr Phe Thr Thr Tyr Asp Thr Asn Gly Arg Tyr Ser
                660                      665                  670
Val Lys Val Arg Ala Leu Gly Gly Val Asn Ala Ala Arg Arg Arg Val
            675                      680                  685
Ile Pro Gln Gln Ser Gly Ala Leu Tyr Ile Pro Gly Trp Ile Glu Asn
            690                      695                  700
Asp Glu Ile Gln Trp Asn Pro Pro Arg Pro Glu Ile Asn Lys Asp Asp
705                      710                      715              720
Val Gln His Lys Gln Val Cys Phe Ser Arg Thr Ser Ser Gly Gly Ser
                    725                      730                  735
Phe Val Ala Ser Asp Val Pro Asn Ala Pro Ile Pro Asp Leu Phe Pro
                740                      745                  750
Pro Gly Gln Ile Thr Asp Leu Lys Ala Glu Ile His Gly Gly Ser Leu
            755                      760                  765
Ile Asn Leu Thr Trp Thr Ala Pro Gly Asp Asp Tyr Asp His Gly Thr
            770                      775                  780
Ala His Lys Tyr Ile Ile Arg Ile Ser Thr Ser Ile Leu Asp Leu Arg
785                      790                      795              800
Asp Lys Phe Asn Glu Ser Leu Gln Val Asn Thr Thr Ala Leu Ile Pro
                    805                      810                  815
Lys Glu Ala Asn Ser Glu Glu Val Phe Leu Phe Lys Pro Glu Asn Ile
                820                      825                  830
Thr Phe Glu Asn Gly Thr Asp Leu Phe Ile Ala Ile Gln Ala Val Asp
            835                      840                  845
Lys Val Asp Leu Lys Ser Glu Ile Ser Asn Ile Ala Arg Val Ser Leu
        850                      855                  860
Phe Ile Pro Pro Gln Thr Pro Pro Glu Thr Pro Ser Pro Asp Glu Thr
865                      870                      875              880
Ser Ala Pro Cys Pro Asn Ile His Ile Asn Ser Thr Ile Pro Gly Ile
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His Ile Leu Lys Ile Met Trp Lys Trp Ile Gly Glu Leu Gln Leu Ser
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<210> 27
<211> 1756

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<212> DNA
<213> Human

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<211> 527
<212> PRT
<213> Human

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            20   25   30
Trp Leu Asn Val Lys Ile Ile Ile Asp Glu Leu Ile Lys Lys Glu His
        35   40   45
Asn Val Thr Val Leu Val Ala Ser Gly Ala Leu Phe Ile Thr Pro Thr
    50   55   60
Ser Asn Pro Ser Leu Thr Phe Glu Ile Tyr Lys Val Pro Phe Gly Lys
65   70   75   80
Glu Arg Ile Glu Gly Val Ile Lys Asp Phe Val Leu Thr Trp Leu Glu
                85   90   95
Asn Arg Pro Ser Pro Ser Thr Ile Trp Arg Phe Tyr Gln Glu Met Ala
            100   105   110

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Lys Val Ile Lys Asp Phe His Met Val Ser Gln Glu Ile Cys Asp Gly
        115   120   125
Val Leu Lys Asn Gln Gln Leu Met Ala Lys Leu Lys Lys Ser Lys Phe
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Glu Val Leu Val Ser Asp Pro Val Phe Pro Cys Gly Asp Ile Val Ala
145   150   155   160
Leu Lys Leu Gly Ile Pro Phe Met Tyr Ser Leu Arg Phe Ser Pro Ala
            165   170   175
Ser Thr Val Glu Lys His Cys Gly Lys Val Pro Tyr Pro Pro Ser Tyr
        180   185   190
Val Pro Ala Val Leu Ser Glu Leu Thr Asp Gln Met Ser Phe Thr Asp
    195   200   205
Arg Ile Arg Asn Phe Ile Ser Tyr His Leu Gln Asp Tyr Met Phe Glu
    210   215   220
Thr Leu Trp Lys Ser Trp Asp Ser Tyr Tyr Ser Lys Ala Leu Gly Arg
225   230   235   240
Pro Thr Thr Leu Cys Glu Thr Met Gly Lys Ala Glu Ile Trp Leu Ile
            245   250   255
Arg Thr Tyr Trp Asp Phe Glu Phe Pro Arg Pro Tyr Leu Pro Asn Phe
            260   265   270
Glu Phe Val Gly Gly Leu His Cys Lys Pro Ala Lys Pro Leu Pro Lys
        275   280   285
Glu Met Glu Glu Phe Ile Gln Ser Ser Gly Lys Asn Gly Val Val Val
    290   295   300
Phe Ser Leu Gly Ser Met Val Lys Asn Leu Thr Glu Glu Lys Ala Asn
305   310   315   320
Leu Ile Ala Ser Ala Leu Ala Gln Ile Pro Gln Lys Val Leu Trp Arg
            325   330   335
Tyr Lys Gly Lys Lys Pro Ala Thr Leu Gly Asn Asn Thr Gln Leu Phe
        340   345   350
Asp Trp Ile Pro Gln Asn Asp Leu Leu Gly His Pro Lys Thr Lys Ala
        355   360   365
Phe Ile Thr His Gly Gly Thr Asn Gly Ile Tyr Glu Ala Ile Tyr His
    370   375   380
Gly Val Pro Met Val Gly Val Pro Met Phe Ala Asp Gln Pro Asp Asn
385   390   395   400
Ile Ala His Met Lys Ala Lys Gly Ala Ala Val Glu Val Asn Leu Asn
            405   410   415
Thr Met Thr Ser Val Asp Leu Leu Ser Ala Leu Arg Thr Val Ile Asn
    420   425   430
Glu Pro Ser Tyr Lys Glu Asn Ala Met Arg Leu Ser Arg Ile His His
    435   440   445
Asp Gln Pro Val Lys Pro Leu Asp Arg Ala Val Phe Trp Ile Glu Phe
    450   455   460
Val Met Arg His Lys Gly Ala Lys His Leu Arg Val Ala Ala His Asp
465   470   475   480
Leu Thr Trp Phe Gln Tyr His Ser Leu Asp Val Ile Gly Phe Leu Leu
            485   490   495
Val Cys Val Thr Thr Ala Ile Phe Leu Val Ile Gln Cys Cys Leu Phe
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Ser Cys Gln Lys Phe Gly Lys Ile Gly Lys Lys Lys Lys Arg Glu
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<211> 1870
<212> DNA
<213> Human

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agccattgca cccagccgat actactatat ccccatttta cagatgagca catgggcaaa 180
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<211> 323
<212> PRT
<213> Human

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Leu Pro Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser
            20   25   30
Val Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val
        35   40   45
Asn Phe Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe
    50   55   60
Asn Pro Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln
65   70   75   80
Gly Gly Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys

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Lys Gly Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr
               100                 105                 110
Lys Val Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu
           115                 120                 125
Pro Leu Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu
       130                 135                 140
Gln Ser Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro
   145                 150                 155                 160
Pro Met Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu
               165                 170                 175
Asn Ser Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val
           180                 185                 190
Pro Tyr Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile
       195                 200                 205
Ile Ile Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn
   210                 215                 220
Phe Lys Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg
225                 230                 235                 240
Met Gly Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp
               245                 250                 255
Gly Ser Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln
           260                 265                 270
Phe Phe Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr
       275                 280                 285
Ala Asn Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe
   290                 295                 300
Gln Arg Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr
305                 310                 315                 320
Val Gln Ile
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